

Fig.1

5'		9		18		27		36		45		54						
	ATG	GAA	ATT	ATT	TCA	TCA	AAA	CTA	TTC	ATT	TTA	TTG	ACT	TTA	GCC	ACT	TCA	AGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Glu	Ile	Ile	Ser	Ser	Lys	Leu	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr	Ser	Ser
		63		72		81		90		99		108						
	TTG	TTA	ACA	TCA	AAC	ATT	TTT	TGT	GCA	GAT	GAA	TTA	GTG	ATG	TCC	AAT	CTT	CAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Ala	Asp	Glu	Leu	Val	Met	Ser	Asn	Leu	His
		117		126		135		144		153		162						
	AGC	AAA	GAA	AAT	TAT	GAC	AAA	TAT	TCT	GAG	CCT	AGA	GGA	TAC	CCA	AAA	GGG	GAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Lys	Glu	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Tyr	Pro	Lys	Gly	Glu
		171		180		189		198		207		216						
	AGA	AGC	CTC	AAT	TTT	GAG	GAA	TTA	AAA	GAT	TGG	GGA	CCA	AAA	AAT	GTT	ATT	AAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp	Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys
		225		234		243		252		261		270						
	ATG	AGT	ACA	CCT	GCA	GTC	AAT	AAA	ATG	CCA	CAC	TCC	TTC	GCC	AAC	TTG	CCA	TTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys	Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu
		279		288		297		306		315		324						
	AGA	TTT	GGG	AGG	AAC	GTT	CAA	GAA	GAA	AGA	AGT	GCT	GGA	GCA	ACA	GCC	AAC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Phe	Gly	Arg	Asn	Val	Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu
		333		342		351		360		369		378						
	CCT	CTG	AGA	TCT	GGA	AGA	AAT	ATG	GAG	GTG	AGC	CTC	GTG	AGA	CGT	GTT	CCT	AAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Pro	Leu	Arg	Ser	Gly	Arg	Asn	Met	Glu	Val	Ser	Leu	Val	Arg	Arg	Val	Pro	Asn
		387		396		405		414		423		432						
	CTG	CCC	CAA	AGG	TTT	GGG	AGA	ACA	ACA	GCC	AAA	AGT	GTC	TGC	AGG	ATG	CTG	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu	
		441		450		459		468		477		486						
	AGT	GAT	TTG	TGT	CAA	GGA	TCC	ATG	CAT	TCA	CCA	TGT	GCC	AAT	GAC	TTA	TTT	TAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Asp	Leu	Cys	Gln	Gly	Ser	Met	His	Ser	Pro	Cys	Ala	Asn	Asp	Leu	Phe	Tyr
		495		504		513		522		531		540						
	TCC	ATG	ACC	TGC	CAG	CAC	CAA	GAA	ATC	CAG	AAT	CCC	GAT	CAA	AAA	CAG	TCA	AGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Met	Thr	Cys	Gln	His	Gln	Glu	Ile	Gln	Asn	Pro	Asp	Gln	Lys	Gln	Ser	Arg

TAA 3'

Fig.2

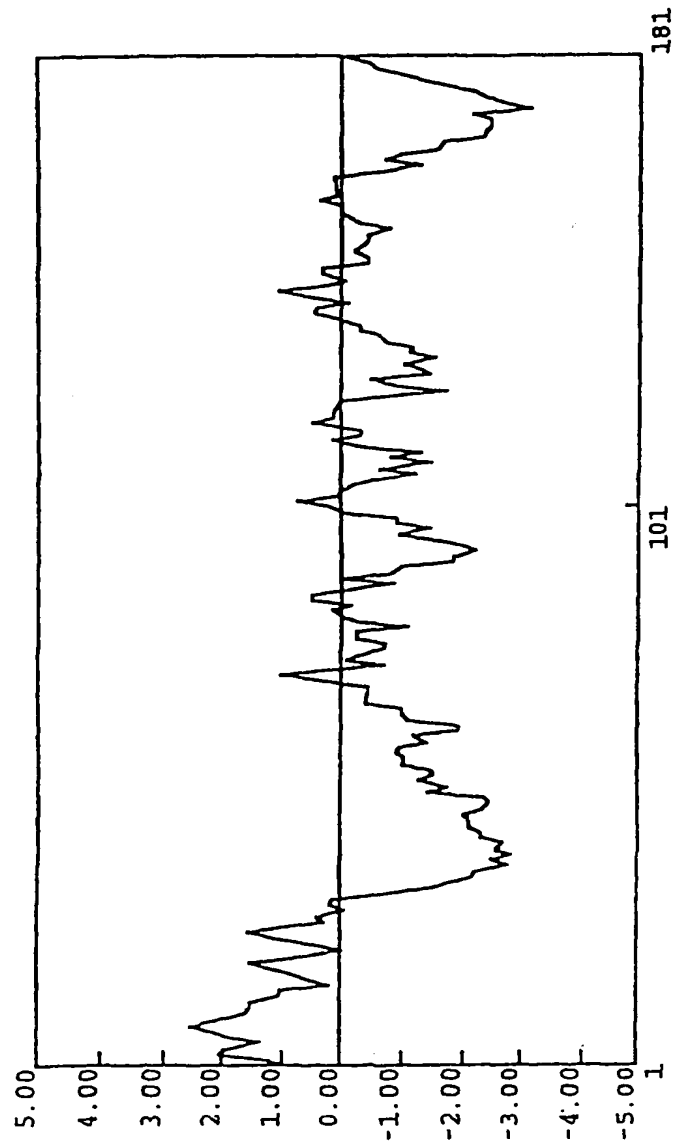


Fig.3

```

5'  ATG  GAA  ATT  ATT  TCA  TCA  AAA  CTA  TTC  ATT  TTA  TTG  ACT  TTA  GCC  ACT  TCA  AGC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Met  Glu  Ile  Ile  Ser  Ser  Lys  Leu  Phe  Ile  Leu  Leu  Thr  Leu  Ala  Thr  Ser  Ser

      9      18      27      36      45      54
    TTG  TTA  ACA  TCA  AAC  ATT  TTT  TGT  GCA  GAT  GAA  TTA  GTG  ATG  TCC  AAT  CTT  CAC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Leu  Leu  Thr  Ser  Asn  Ile  Phe  Cys  Ala  Asp  Glu  Leu  Val  Met  Ser  Asn  Leu  His

      63      72      81      90      99      108
    AGC  AAA  GAA  AAT  TAT  GAC  AAA  TAT  TCT  GAG  CCT  AGA  GGA  TAC  CCA  AAA  GGG  GAA
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Ser  Lys  Glu  Asn  Tyr  Asp  Lys  Tyr  Ser  Glu  Pro  Arg  Gly  Tyr  Pro  Lys  Gly  Glu

      117      126      135      144      153      162
    AGA  AGC  CTC  AAT  TTT  GAG  GAA  TTA  AAA  GAT  TGG  GGA  CCA  AAA  AAT  GTT  ATT  AAG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Arg  Ser  Leu  Asn  Phe  Glu  Glu  Leu  Lys  Asp  Trp  Gly  Pro  Lys  Asn  Val  Ile  Lys

      171      180      189      198      207      216
    ATG  AGT  ACA  CCT  GCA  GTC  AAT  AAA  ATG  CCA  CAC  TCC  TTC  GCC  AAC  TTG  CCA  TTG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Met  Ser  Thr  Pro  Ala  Val  Asn  Lys  Met  Pro  His  Ser  Phe  Ala  Asn  Leu  Pro  Leu

      225      234      243      252      261      270
    AGA  TTT  GGG  AGG  AAC  GTT  CAA  GAA  GAA  AGA  AGT  GCT  GGA  GCA  ACA  GCC  AAC  CTG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Arg  Phe  Gly  Arg  Asn  Val  Gln  Glu  Glu  Arg  Ser  Ala  Gly  Ala  Thr  Ala  Asn  Leu

      279      288      297      306      315      324
    CCT  CTG  AGA  TCT  GGA  AGA  AAT  ATG  GAG  GTG  AGC  CTC  GTG  AGA  CGT  GTT  CCT  AAC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Pro  Leu  Arg  Ser  Gly  Arg  Asn  Met  Glu  Val  Ser  Leu  Val  Arg  Arg  Val  Pro  Asn

      333      342      351      360      369      378
    CTG  CCC  CAA  AGG  TTT  GGG  AGA  ACA  ACA  ACA  GCC  AAA  AGT  GTC  TGC  AGG  ATG  CTG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Leu  Pro  Gln  Arg  Phe  Gly  Arg  Thr  Thr  Thr  Ala  Lys  Ser  Val  Cys  Arg  Met  Leu

      387      396      405      414      423      432
    AGT  GAT  TTG  TGT  CAA  GGA  TCC  ATG  CAT  TCA  CCA  TGT  GCC  AAT  GAC  TTA  TTT  TAC
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Ser  Asp  Leu  Cys  Gln  Gly  Ser  Met  His  Ser  Pro  Cys  Ala  Asn  Asp  Leu  Phe  Tyr

      441      450      459      468      477      486
    TCC  ATG  ACC  TGC  CAG  CAC  CAA  GAA  ATC  CAG  AAT  CCC  GAT  CAA  AAA  CAG  TCA  AGG
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Ser  Met  Thr  Cys  Gln  His  Gln  Glu  Ile  Gln  Asn  Pro  Asp  Gln  Lys  Gln  Ser  Arg

      495      504      513      522      531      540
    AGA  CTG  CTA  TTC  AAG  AAA  ATA  GAT  GAT  GCA  GAA  TTG  AAA  CAA  GAA  AAA  TAA  3'
    ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
    Arg  Leu  Leu  Phe  Lys  Lys  Ile  Asp  Asp  Ala  Glu  Leu  Lys  Gln  Glu  Lys  ***

```

Fig.4

		9		18		27		36		45		54						
5'	ATG	GAA	ATT	ATT	TCA	TTA	AAA	CGA	TTC	ATT	TTA	TTG	ATG	TTA	GCC	ACT	TCA	AGC
	Met	Glu	Ile	Ile	Ser	Leu	Lys	Arg	Phe	Ile	Leu	Leu	Met	Leu	Ala	Thr	Ser	Ser
		63		72		81		90		99		108						
	TTG	TTA	ACA	TCA	AAC	ATC	TTC	TGC	ACA	GAC	GAA	TCA	AGG	ATG	CCC	AAT	CTT	TAC
	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Thr	Asp	Glu	Ser	Arg	Met	Pro	Asn	Leu	Tyr
		117		126		135		144		153		162						
	AGC	AAA	AAG	AAT	TAT	GAC	AAA	TAT	TCC	GAG	CCT	AGA	GGA	GAT	CTA	GGC	TGG	GAG
	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Asp	Leu	Gly	Trp	Glu
		171		180		189		198		207		216						
	AAA	GAA	AGA	AGT	CTT	ACT	TTT	GAA	GAA	GTA	AAA	GAT	TGG	GCT	CCA	AAA	ATT	AAG
	Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val	Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys
		225		234		243		252		261		270						
	ATG	AAT	AAA	CCT	GTA	GTC	AAC	AAA	ATG	CCA	CCT	TCT	GCA	GCC	AAC	CTG	CCA	CTG
	Met	Asn	Lys	Pro	Val	Val	Asn	Lys	Met	Pro	Pro	Ser	Ala	Ala	Asn	Leu	Pro	Leu
		279		288		297		306		315		324						
	AGA	TTT	GGG	AGG	AAC	ATG	GAA	GAA	GAA	AGG	AGC	ACT	AGG	GCG	ATG	GCC	CAC	CTG
	Arg	Phe	Gly	Arg	Asn	Met	Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu
		333		342		351		360		369		378						
	CCT	CTG	AGA	CTC	GGA	AAA	AAT	AGA	GAG	GAC	AGC	CTC	TCC	AGA	TGG	GTC	CCA	AAT
	Pro	Leu	Arg	Leu	Gly	Lys	Asn	Arg	Glu	Asp	Ser	Leu	Ser	Arg	Trp	Val	Pro	Asn
		387		396		405		414		423		432						
	CTG	CCC	CAG	AGG	TTT	GGA	AGA	ACA	ACA	ACA	GCC	AAA	AGC	ATT	ACC	AAG	ACC	CTG
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu
		441		450		459		468		477		486						
	AGT	AAT	TTG	CTC	CAG	CAG	TCC	ATG	CAT	TCA	CCA	TCT	ACC	AAT	GGG	CTA	CTC	TAC
	Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	Gly	Leu	Leu	Tyr
		495		504		513		522		531		540						
	TCC	ATG	GCC	TGC	CAG	CCC	CAA	GAA	ATC	CAG	AAT	CCT	GGT	CAA	AAG	AAC	CTA	AGG
	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln	Lys	Asn	Leu	Arg
		549		558		567		576		585								
	AGA	CGG	GGA	TTC	CAG	AAA	ATA	GAT	GAT	GCA	GAA	TTG	AAA	CAA	GAA	AAA	TAA	3'
	Arg	Arg	Gly	Phe	Gln	Lys	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	***	

Gly Ala Met Lys Leu ***

Fig.6

hLPLRF.aa	1	MEIIS	KRFI	LI	LT	AT	SS	LL	TS	NI	F	CA	DEL	V	S	N	L	H	S	K	E	N	Y	D	K	Y	S	E	P	R	G	50																		
bLPLRF.aa	1	MEIIS	KRFI	LI	LT	AT	SS	LL	TS	NI	F	CA	DES	R	M	P	N	L	H	S	K	E	N	Y	D	K	Y	S	E	P	R	G	50																	
rLPLRF.aa	1	MEIIS	KRFI	LI	LT	AT	SS	FL	TS	NI	F	CA	DEL	M	E	F	H	S	K	E	G	Y	K	Y	Q	I	R	G	I			50																		
hLPLRF.aa	51	--Y	P	K	G	---	E	R	S	L	F	E	E	L	K	D	W	G	P	K	N	V	I	K	M	S	T	E	A	N	L	P	L	R	F	G	R	N	100											
bLPLRF.aa	51	L	G	W	E	K	---	E	R	S	L	F	E	E	V	K	W	A	P	K	---	I	K	M	N	K	E	V	A	N	L	P	L	R	F	G	R	N	100											
rLPLRF.aa	51	---	P	K	G	V	K	E	R	S	L	F	E	E	L	K	D	W	G	A	K	K	I	K	M	S	E	A	P	A	N	L	P	L	R	F	G	R	N	100										
hLPLRF.aa	101	V	Q	E	R	S	A	G	A	T	A	N	L	P	L	R	S	G	R	N	M	E	V	S	L	V	R	R	V	P	N	L	P	Q	R	F	G	R	T	T	A	K	S	V	C	R	M	L	S	150
bLPLRF.aa	101	M	E	E	R	S	I	F	R	A	M	A	N	L	P	L	R	S	G	R	N	R	E	I	S	L	S	R	V	P	N	L	P	Q	R	F	G	R	T	T	A	K	S	I	T	K	T	L	S	150
rLPLRF.aa	101	I	E	D	R	S	P	R	A	R	A	N	M	---	---	---	---	---	---	---	E	A	G	T	S	H	F	E	S	L	P	Q	R	F	G	R	T	T	A	R	R	I	T	K	T	L	A	150		
hLPLRF.aa	151	D	I	Q	S	M	H	S	E	C	A	N	L	E	Y	S	M	T	C	O	H	E	I	Q	N	E	D	Q	K	S	R	R	L	L	E	K	K	I	D	D	A	E	L	K	Q	E	200			
bLPLRF.aa	151	N	L	Q	S	M	H	S	E	S	I	N	G	L	L	Y	S	M	A	C	O	H	E	I	Q	N	E	D	Q	K	N	L	R	R	R	E	F	Q	K	I	D	D	A	E	L	K	Q	E	200	
rLPLRF.aa	151	G	L	P	K	S	L	H	S	E	A	S	S	E	S	L	Y	A	M	I	R	O	H	E	I	Q	S	P	G	Q	E	P	R	R	V	E	T	E	I	D	D	A	E	R	K	Q	E	200		
hLPLRF.aa	201	K	*	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	250	
bLPLRF.aa	201	K	*	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	250		
rLPLRF.aa	201	K	I	G	N	L	Q	P	V	L	Q	G	A	M	K	L	*	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	250		

Fig.7

1	TTTAGACTTAGACGAAATGGAAATTATTTTCATTAAAACGATTCATTTTATTGACTGTG	58
1	MetGluIleIleSerLeuLysArgPheIleLeuLeuThrVal	14
59	GCAACTTCAAGCTTCTTAACATCAAACACCTTCTGTACAGATGAGTTCATGATGCCTCAT	118
15	AlaThrSerSerPheLeuThrSerAsnThrPheCysThrAspGluPheMetMetProHis	34
119	TTTCACAGCAAAGAAGGTGACGGAAAATACTCCCAGCTGAGAGGAATCCCAAAAGGGGAA	178
35	PheHisSerLysGluGlyAspGlyLysTyrSerGlnLeuArgGlyIleProLysGlyGlu	54
179	AAGGAAAGAAGTGTCAAGTTTCAAGAACTAAAAGATTGGGGGGCAAAGAATGTTATTAAG	238
55	LysGluArgSerValSerPheGlnGluLeuLysAspTrpGlyAlaLysAsnValIleLys	74
239	ATGAGTCCAGCCCCTGCCAACAAAGTGCCCCACTCAGCAGCCAACCTGCCCTGAGATTT	298
75	MetSerProAlaProAlaAsnLysValProHisSerAlaAlaAsnLeuProLeuArgPhe	94
299	GGAAGGACCATAGATGAGAAAAGAAGCCCCGCAGCACGGGTCAACATGGAGGCAGGGACC	358
95	GlyArgThrIleAspGluLysArgSerProAlaAlaArgValAsnMetGluAlaGlyThr	114
359	AGGAGCCATTTCCCCAGCCTGCCCCAAAGGTTTGGGAGAACAACAGCCAGAAGCCCCAAG	418
115	ArgSerHisPheProSerLeuProGlnArgPheGlyArgThrThrAlaArgSerProLys	154
419	ACACCCGCTGATTTGCCACAGAAACCCCTGCACTCACTGGGCTCCAGCGAGTTGCTCTAC	538
135	ThrProAlaAspLeuProGlnLysProLeuHisSerLeuGlySerSerGluLeuLeuTyr	154
479	GTCATGATCTGCCAGCACCAAGAAATTCAGAGTCCTGGTGGAAAGCGAACGAGGAGAGGA	538
155	ValMetIleCysGlnHisGlnGluIleGlnSerProGlyGlyLysArgThrArgArgGly	174
539	GCGTTTGTGGAAACAGATGATGCAGAAAGGGAAACCAGAAAAATAGGAAACTCGAGCCCCG	598
175	AlaPheValGluThrAspAspAlaGluArgLysProGluLys***	188
599	ACTTCAAGAGGCTACGGAGC	618
188		188

Fig.8

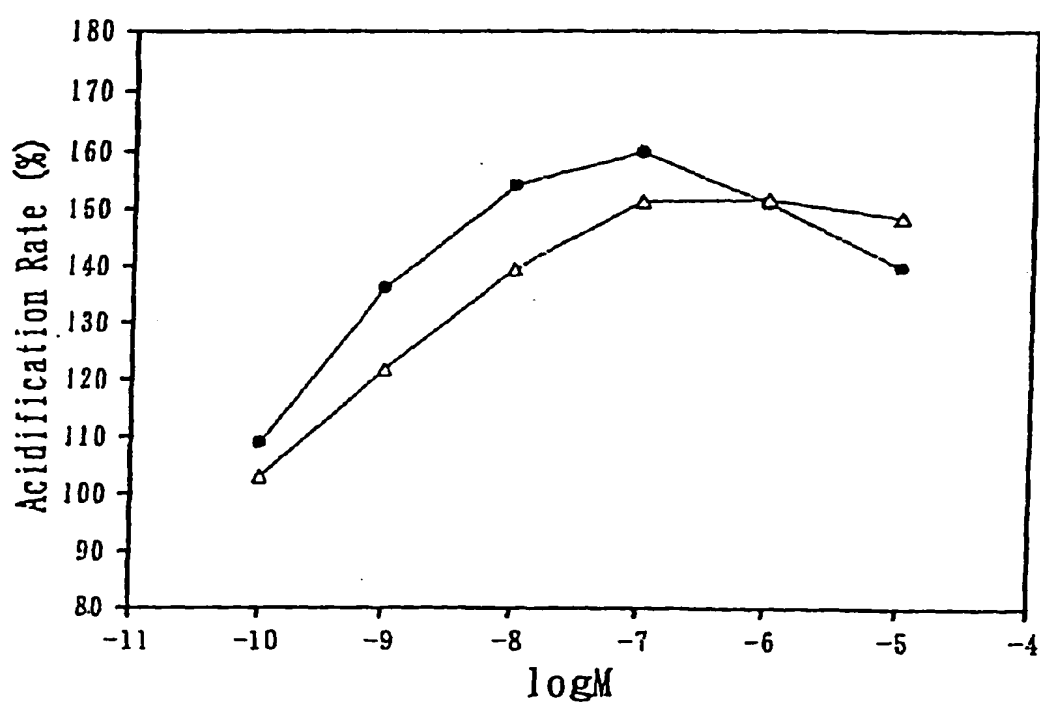


Fig.9

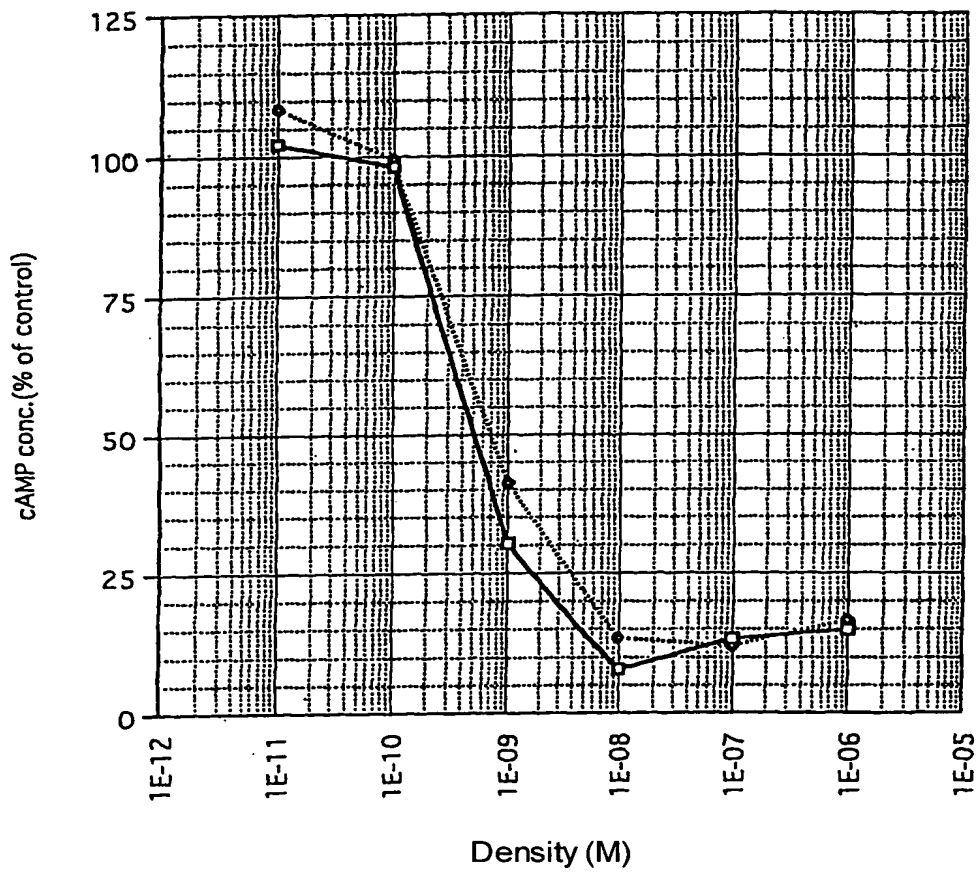


Fig.10

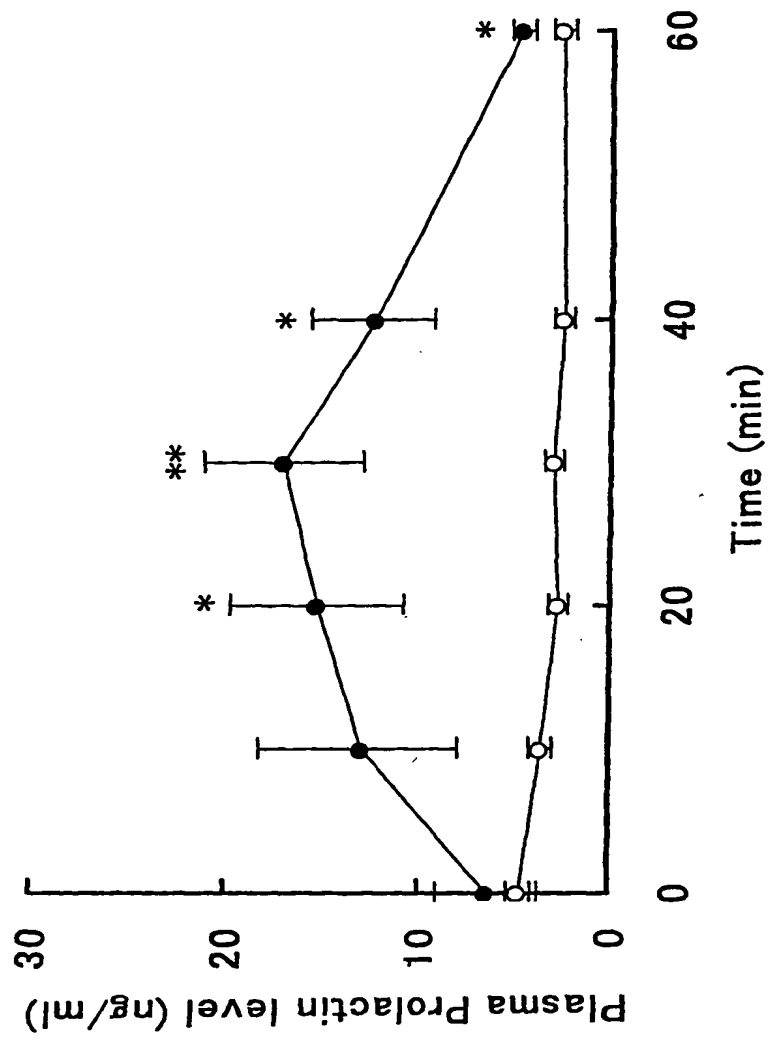
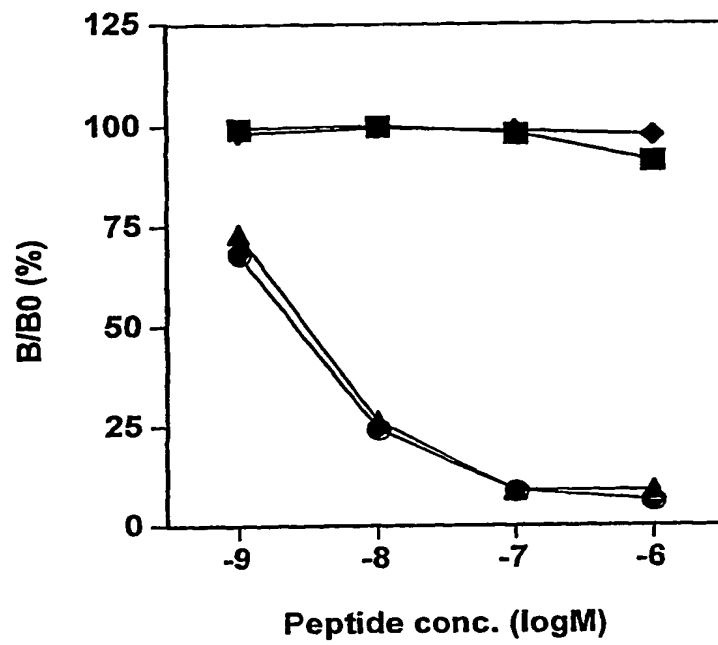


Fig.11



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Fig.12

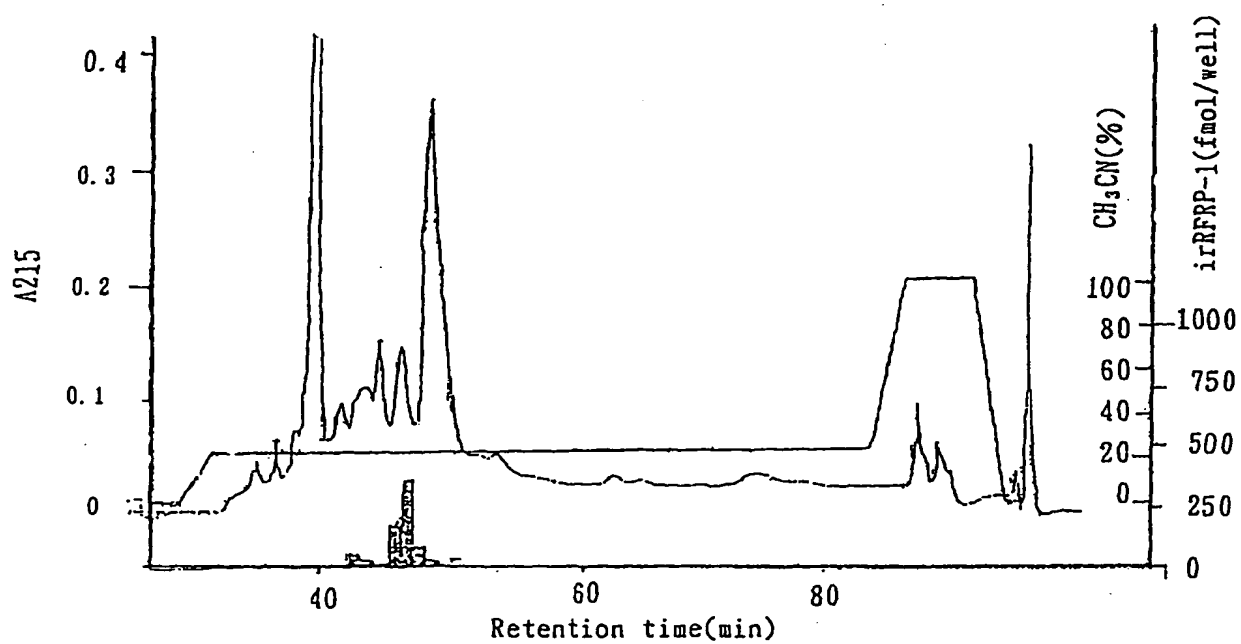


Fig.13

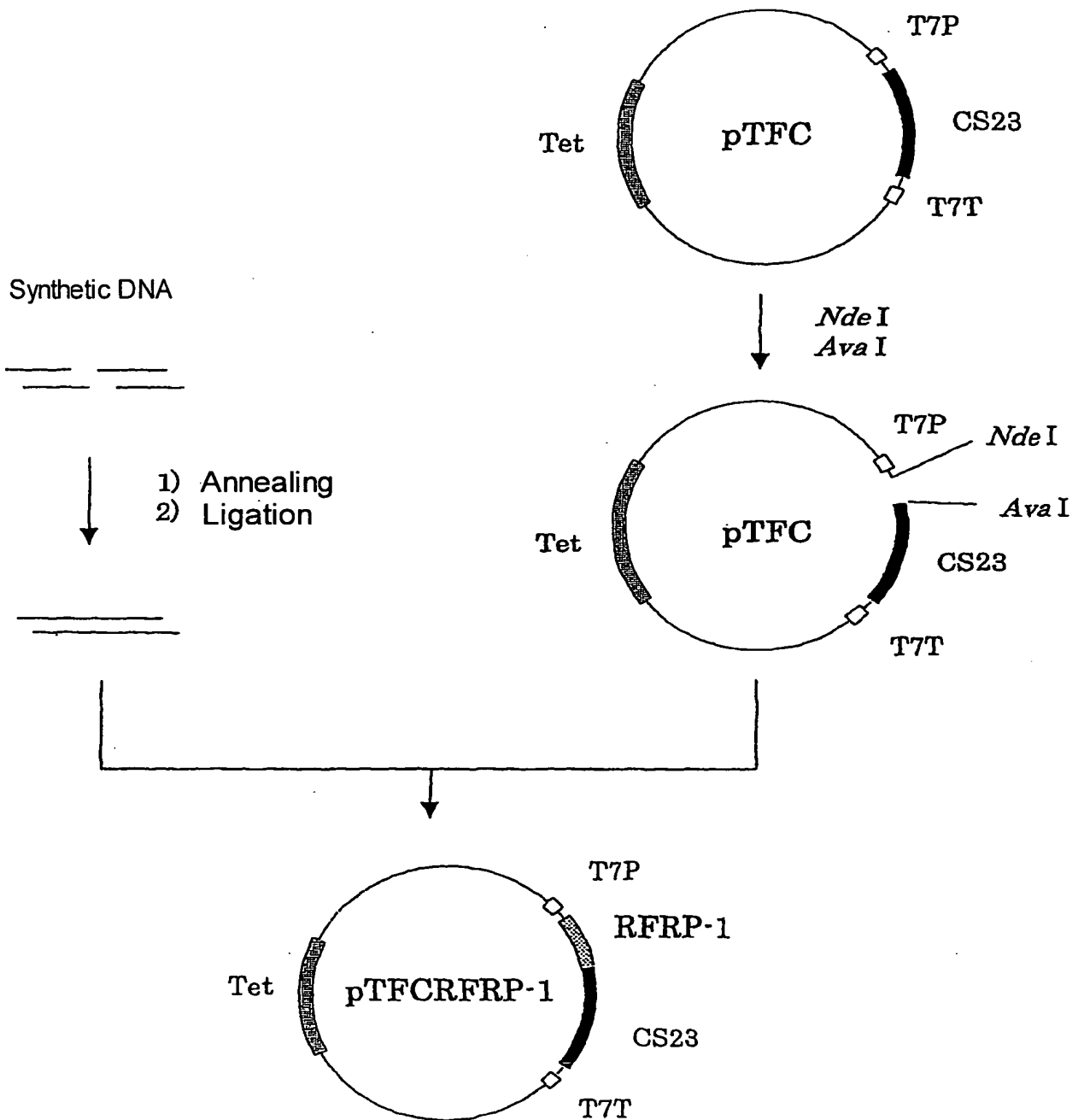


Fig.14

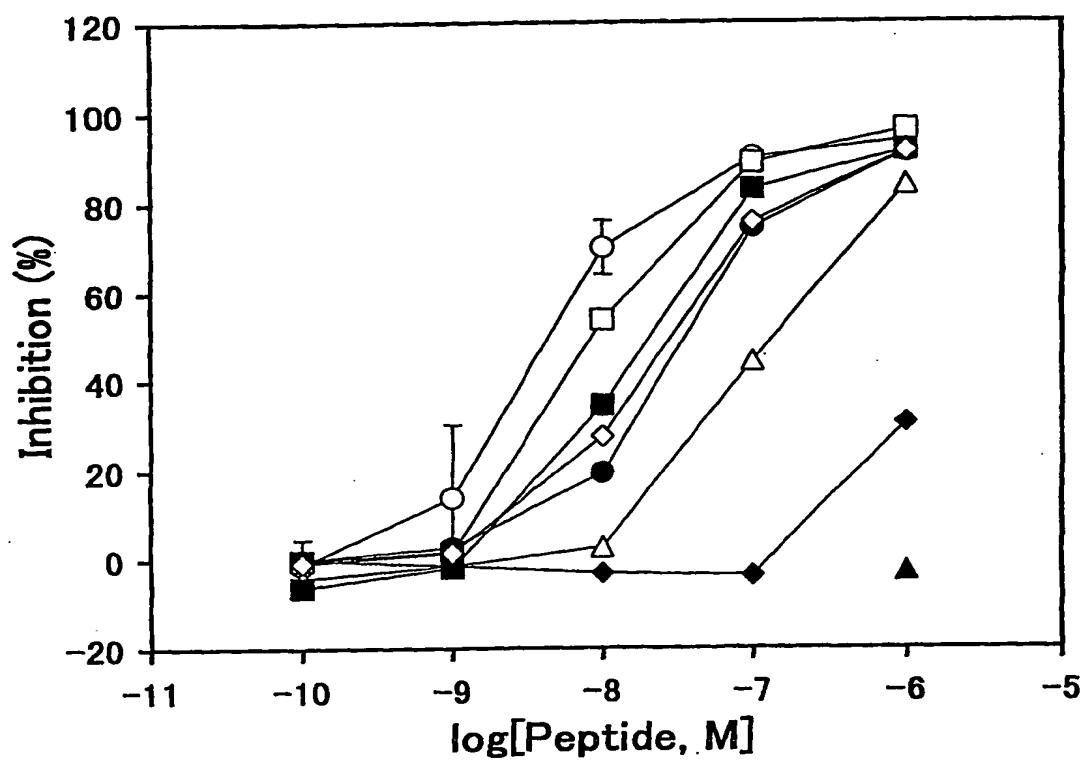


Fig.15

